

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/936,702

DATE: 10/04/2001

TIME: 14:41:19

Input Set : A:\60771 seq.txt

Output Set: N:\CRF3\10042001\I936702.raw

3 <110> APPLICANT: Berger, et al.
 5 <120> TITLE OF INVENTION: NOVEL CHIMERIC PROTEIN FOR PREVENTION AND TREATMENT OF
 6 HIV INFECTION
 8 <130> FILE REFERENCE: 4239-60771
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/936,702
 C--> 11 <141> CURRENT FILING DATE: 2001-09-13
 13 <150> PRIOR APPLICATION NUMBER: PCT/US00/06946
 14 <151> PRIOR FILING DATE: 2000-03-16
 16 <150> PRIOR APPLICATION NUMBER: 60/124,681
 17 <151> PRIOR FILING DATE: 1999-03-16
 19 <160> NUMBER OF SEQ ID NOS: 11
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 5
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Description of Artificial Sequence: linker peptide ✓
 31 <400> SEQUENCE: 1
 32 Gly Gly Gly Gly Ser
 33 1 5
 36 <210> SEQ ID NO: 2
 37 <211> LENGTH: 35
 38 <212> TYPE: PRT
 39 <213> ORGANISM: Artificial Sequence
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: Description of Artificial Sequence: seven repeat ✓
 43 polypeptide linker
 45 <400> SEQUENCE: 2
 46 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 47 1 5 10 15
 49 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 50 20 25 30
 52 Gly Gly Ser
 53 35
 56 <210> SEQ ID NO: 3
 57 <211> LENGTH: 508
 58 <212> TYPE: PRT
 59 <213> ORGANISM: Artificial Sequence
 61 <220> FEATURE:
 62 <223> OTHER INFORMATION: Description of Artificial Sequence: CD4-scFv(17b) ✓
 64 <400> SEQUENCE: 3
 65 Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Val Leu Gln Leu
 66 1 5 10 15
 68 Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys
 69 20 25 30
 71 Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser

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72          35          40          45
74 Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
75          50          55          60
77 Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
78 65          70          75          80
80 Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
81          85          90          95
83 Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
84          100          105          110
86 Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
87          115          120          125
89 Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
90          130          135          140
92 Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
93 145          150          155          160
95 Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
96          165          170          175
98 Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
99          180          185          190
101 Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser
102          195          200          205
104 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
105          210          215          220
107 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
108 225          230          235          240
110 Gly Gly Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Glu Val Lys Lys
111          245          250          255
113 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Asp Thr Phe
114          260          265          270
116 Ile Arg Tyr Ser Phe Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
117          275          280          285
119 Glu Trp Met Gly Arg Ile Ile Thr Ile Leu Asp Val Ala His Tyr Ala
120          290          295          300
122 Pro His Leu Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
123 305          310          315          320
125 Thr Val Tyr Leu Glu Leu Arg Asn Leu Arg Ser Asp Asp Thr Ala Val
126          325          330          335
128 Tyr Phe Cys Ala Gly Val Tyr Glu Gly Glu Ala Asp Glu Gly Glu Tyr
129          340          345          350
131 Asp Asn Asn Gly Phe Leu Lys His Trp Gly Gln Gly Thr Leu Val Thr
132          355          360          365
134 Val Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
135          370          375          380
137 Gly Ser Glu Leu Glu Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Ser
138 385          390          395          400
140 Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Ser Val Ser
141          405          410          415
143 Ser Asp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu
144          420          425          430

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146 Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Val Pro Ala Arg Phe
 147 435 440 445
 149 Ser Gly Ser Gly Ser Gly Ala Glu Phe Thr Leu Thr Ile Ser Ser Leu
 150 450 455 460
 152 Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp
 153 465 470 475 480
 155 Pro Pro Arg Tyr Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Leu
 156 485 490 495
 158 Val Pro Arg Gly Ser Gly His His His His His His
 159 500 505
 162 <210> SEQ ID NO: 4
 163 <211> LENGTH: 1440
 164 <212> TYPE: DNA
 165 <213> ORGANISM: Artificial Sequence
 167 <220> FEATURE:
 168 <223> OTHER INFORMATION: Description of Artificial Sequence: CD4-scFv(17b)
 170 <400> SEQUENCE: 4
 171 atgaaccggg gagtcccttt taggcacttg cttctggtgc tgcaactggc gtcctcccca 60
 172 gcagccactc agggaaagaa agtgggtgctg ggcaaaaaag gggatacagt ggaactgacc 120
 173 tgtacagctt cccagaagaa gagcatacaa ttccactgga aaaactccaa ccagataaag 180
 174 attctgggaa atcagggctc cttcttaact aaaggtccat ccaagctgaa tgatcgcgct 240
 175 gactcaagaa gaagcctttg ggaccaagga aacttcccc tgatcatcaa gaatcttaag 300
 176 atagaagact cagataactta catctgtgaa gtggaggacc agaaggagga ggtgcaattg 360
 177 ctagtgttcg gattgactgc caactctgac acccacctgc ttcaggggca gacgctgacc 420
 178 ctgaccttgg agagcccccc tggtagtagc ccctcagtgc aatgtaggag tccaaggggt 480
 179 aaaaacatac agggggggaa gaccctctcc gtgtctcagc tggagctcca ggatagtggc 540
 180 acctggacat gcaactgtctt gcagaaccag aagaaggttg agttcaaaat agacatcgtg 600
 181 gtgctagctt tccagaaggc ctccggaggt ggcggtagtg ggggaggcgg ttcaggcggg 660
 182 ggtggatccg gtggcggagg gtcgggcggg ggtggaagcg ggggtggcgg ctccggaggc 720
 183 ggaggttcac aggtgcagct gctcgagtct ggggctgagg tgaagaagcc tgggtcctcg 780
 184 gtgaaggtct cctgcaaggc ctctggagac accttcacat gatatagttt tacctgggtg 840
 185 cgacaggccc ctggacaagg ccttgagtgg atgggaagga tcatcactat ccttgatgta 900
 186 gcacactacg caccgcacct ccagggcaga gtcacgatta ccgcggaaca gtccacgagc 960
 187 acagtctacc tggagctgcg gaatctaaga tctgacgata cggccgtata tttctgtgcg 1020
 188 ggagtgtacg agggagaggc ggacgagggg gaatatgata ataatgggtt tctgaacat 1080
 189 tggggccagg gaacctggt caccgtcacc tcaggtggcg gtggctccg aggtggtggg 1140
 190 agcgggtggc gcggatctga actcgagttg acgcagctc cagccaccct gtctgtgtct 1200
 191 ccaggggaaa gagccaccct ctctgcagg gccagtgaga gtgttagtag cgacttagcc 1260
 192 tggtagcagc agaaacctgg ccaggctccc aggtctctca tatatggtgc atccaccagg 1320
 193 gccaccggtg tcccagccag gttcagtggc agtgggtctg gggcagaatt cactctcacc 1380
 194 atcagcagcc tgcagtctga agattttgca gtttattact gtcagcagta caataactgg 1440
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 198 <211> LENGTH: 127
 199 <212> TYPE: DNA
 200 <213> ORGANISM: Artificial Sequence
 202 <220> FEATURE:
 203 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
 204 oligonucleotide
 206 <400> SEQUENCE: 5

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207 cctccggagg tggcggtagt gggggaggcg gttcaggcgg aggtggatcc ggaggcggag 60
208 ggtcgggcgg ggggtggaagc ggggggtggcg gctctggtgg cggaggtacc actagttaa 120
209 tgagtag
212 <210> SEQ ID NO: 6
213 <211> LENGTH: 39
214 <212> TYPE: PRT
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Description of Artificial Sequence: peptide ✓
219     encoded by SEQ ID NO: 5
221 <400> SEQUENCE: 6
222 Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
223   1             5             10             15
225 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
226             20             25             30
228 Gly Gly Gly Gly Thr Thr Ser
229   35
232 <210> SEQ ID NO: 7
233 <211> LENGTH: 103
234 <212> TYPE: DNA
235 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Description of Artificial Sequence: primer ✓
240 <400> SEQUENCE: 7
241 ttttatggat ccggtggcgg agggtcgggc gggggtggaa gcgggggtgg cggctccgga 60
242 ggcggaggtt cacaggtgca gctgctcgag tctggggctg agg
243             20             25             30
245 <210> SEQ ID NO: 8
246 <211> LENGTH: 32
247 <212> TYPE: PRT
248 <213> ORGANISM: Artificial Sequence
250 <220> FEATURE:
251 <223> OTHER INFORMATION: Description of Artificial Sequence: peptide ✓
252     encoded for by SEQ ID NO: 7
254 <400> SEQUENCE: 8
255 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
256   1             5             10             15
258 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Glu
259             20             25             30
265 <210> SEQ ID NO: 9
266 <211> LENGTH: 65
267 <212> TYPE: DNA
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Description of Artificial Sequence: primer ✓
273 <400> SEQUENCE: 9
274 taatttatcg atcacgtgac tagtcctagg cccgggtcaa tgatgatgat gatgatggcc 60
275 gctgc
278 <210> SEQ ID NO: 10
279 <211> LENGTH: 8

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280 <212> TYPE: PRT
281 <213> ORGANISM: Artificial Sequence
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Description of Artificial Sequence: peptide ✓
285     encoded for by SEQ ID NO: 9
287 <400> SEQUENCE: 10
288 Ser Gly His His His His His His
289   1                               5
292 <210> SEQ ID NO: 11
293 <211> LENGTH: 131
294 <212> TYPE: DNA
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:
298 <223> OTHER INFORMATION: Description of Artificial Sequence: reverse ✓
299     oligonucleotide
301 <400> SEQUENCE: 11
302 ctagctactc acttaactag tggtagctcc gccacctgag ccgccacccc cgcttccacc 60
303 ccccgccgga cctccgcct ccggtccac ctccgcctga accgcctccc cactaccgcc 120
304 acctccggag g                                     131

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

09/04/2001 14:41:20